Claims:

1. A computer system comprising at least one database correlating the presence of at least one mutation in a human immunodeficiency virus (HIV) reverse transcriptase and a change in susceptibility of at least one strain of HIV to a reverse transcriptase inhibitor, comprising at least one record corresponding to a correlation between at least one mutation 194G in said reverse transcriptase, and treatment with at least a reverse transcriptase inhibitor.

2. A method for evaluating the effectiveness of a reverse transcriptase inhibitor as an antiviral therapy for a patient infected with at least one mutant HIV straincomprising:

   (i) collecting a sample from an HIV-infected patient;

   (ii) determining whether the sample comprises a nucleic acid encoding HIV reverse transcriptase having at least one mutation 194G;

   (iii) correlating the presence of said at least one mutation of step (ii) to a change in effectiveness of said reverse transcriptase inhibitor.

3. A method for identifying a drug effective against mutant HIV reverse transcriptase, comprising:

   (i) providing a HIV reverse transcriptase nucleic acid comprising at least one mutation 194G;

   (ii) recombining said nucleic acid of step (i) into a proviral nucleic acid deleted for said sequence to generate a recombinant HIV virus;

   (iii) determining a phenotypic response of said drug to said HIV reverse transcriptase; and

   (iv) identifying a drug effective against mutant HIV based on the phenotypic response of step (iii) .

4. A method for identifying a drug effective against mutant HIV reverse transcriptase, comprising:

   (i) providing a HIV reverse transcriptase comprising at least one mutation 194G;

   (ii) determining the activity of said drug on said HIV reverse transcriptase;

   (iii) determining the activity of said drug on wild type HIV reverse transcriptase;

   (iv) determining the ratio of the activity determined in step (iii) over the activity

determined in step (ii);

(v) identifying an effective drug against mutant HIV based on the ratio of step (iv).

5. A method for evaluating a change in viral drug susceptibility comprising:

(i) collecting a sample from an HIV-infected patient;

5   (ii) determining whether the sample comprises a HIV reverse transcriptase having at least one mutation 194G;

(iii) correlating the presence of said at least one mutation of step (ii) to a change in viral drug susceptibility.

10   6. A method for evaluating a change in viral drug susceptibility, comprising:

(i) providing an HIV comprising a reverse transcriptase comprising at least one mutation 194G;

(ii) determining a phenotypic response of said virus to said drug; and

(iii) correlating the phenotypic response of step (ii) to a change in viral drug

15   susceptibility.

7. A method for evaluating a change in drug effectiveness against mutant HIV reverse transcriptase, comprising:

(i)   providing a HIV reverse transcriptase comprising at least one mutation 194G;

20   (ii) determining the activity of said drug on said reverse transciptase;

(iii) determining the activity of said drug on wild type HIV reverse transcriptase and;

(iv) determining the ratio of the activity determined in step (iii) over the activity determined in step (ii);

25   (v) identifying an effective drug against mutant HIV based on the ratio of step (iv).

8. A vector for performing phenotypic analysis comprising an HIV sequence having at least one mutation 194G in the HIV reverse transcriptase.

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9. An isolated and purified HIV reverse transcriptase sequence having at least one mutation 194G, wherein said at least one mutation in said sequence correlates to a fold change in susceptibility towards a HIV reverse transcriptase inhibitor.

35   10. An isolated and purified oligonucleotide comprising a HIV reverse transcriptase sequence of 5 to 100 bases for in vitro diagnosis of viral drug resistance,

characterized in that said oligonucleotide comprises at least one mutation 194G.